WHAT IS CLAIMED IS:

1. A method of determining the functional homology between two agents, the method comprising:

deriving a biological dataset profile comprising output from 2 or more parameters, from an experimental system for a test agent;

generating a prediction envelope from a control biological dataset profile, which prediction envelope provides upper and lower limits for experimental variation;

wherein a test agent profile is considered to be different than the control if at least one parameter value of the profile exceeds the prediction envelope limits that correspond to a predefined level of significance.

2. The method according to Claim 1, wherein said test agent is a genetic agent.

3. The method according to Claim 1, wherein said agent is a chemical or biological agent.

4. The method according to Claim 1, wherein said biological dataset profile comprises readouts from multiple cellular parameters resulting from exposure of cells to biological factors in the absence or presence of a test agent.

5. The method according to Claim 4, wherein said system comprises a plurality of samples of a single cell type or types in a common biologically relevant context; comprising at least one control in the absence of the test agent.

6. The method according to Claim 5, wherein a plurality of systems are concatenated for simultaneous analysis.

7. The method according to Claim 6, further comprising the step of displaying relationships between two or more agents after non-supervised hierarchical clustering.

8. The method according to Claim 1, wherein said biological dataset profile from an experimental system for a test agent; and said control biological dataset profile are normalized by the method comprising:

obtaining a mean value for each parameter;

dividing the mean parameter value by the mean parameter value from a negative control sample to generate a ratio;

transforming said ratio.

9. The method according to Claim 8, wherein said control prediction envelope is non-centered, and generated by the method comprising:

creating a 1-standard deviation envelope around the profile of the combined means for each measured values for parameters;

moving the envelope lines in a parallel fashion outwards until a predetermined number of control profiles are completely contained within the envelope lines; and a user specified number has at least one of the measured parameters outside the envelope lines.

10. The method according to Claim 8, wherein said control prediction envelope is centered, and generated by the method comprising:

determining the mean from two control point estimates;

subtracting the mean from the two control point estimates to center the points;

combining the points from all parameters of a system to obtain centered profiles.

11. The method according to Claim 10, wherein said control prediction envelope further comprises a third control curve.

12. The method according to Claim 10, wherein said control prediction envelope is centered, and generated by the method comprising:

calculating a covariance matrix of a set of centered profile

forming a quadratic form of profile vector and the covariance matrix to obtain a single numerical value that represents the distance of each control profile from the center of all control profiles.

13. The method according to Claim 8, wherein normalized test agent profiles are used to generate a trusted profile, the method comprising:

obtaining an initial trusted profile by averaging N datasets of profiles from N experiments;

classifying X number of datasets that utilize the same experimental system, but which have not been included in the averaging process to generate the initial trusted profile;

plotting the classification error;

establishing a value for N that minimizes classification error;

generating a trusted profile using said value of N that minimizes classification error.

14. The method according to Claim 8, further comprising the step of determining the false discovery rate, by the method comprising:

generating a set of null distributions of dissimilarity values.

15. The method according to Claim 14, wherein said generating a set of null distributions comprises:

permuting the values of each profile for all available profiles;

calculating the pairwise correlation coefficients for all profiles;

calculating the probability density function of the correlation coefficients for this permutation; and repeating the procedure for N times; and

using N null distributions to calculate a measure of the count of correlation coefficient values whose values exceed the value obtained from the experimentally observed distribution for given significance level.

16. The method according to Claim 7, wherein a Pearson correlation is employed as the clustering metric.

17. The method according to Claim 16, wherein multidimensional scaling is applied in one, two or three dimensions.

18. The method according to Claim 17, wherein a combination of multidimensional scaling and pivoting is used to move high correlations toward the diagonal

19. The method according to Claim 18, wherein the results of said multidimensional scaling and pivoting are displayed as a network.

20. The method according to Claim 19, wherein the display of information further comprises other classification schemes to aid in analysis.

21. The method according to Claim 20, wherein additional information is conveyed by the use of multiple visualization windows.

22. The method according to Claim 21, wherein additional information is conveyed by the use of stereo visualization.

23. The method according to Claim 19, where the field of view of said display is restricted to a portion of the complete set, and where distances are optimized for those points currently visualized.

24. A system for the determining the functional homology between two agents, the system comprising:

a data processor comprising software for determination of functional homology between two agents by the algorithm comprising:

deriving a biological dataset profile from an experimental system for a test agent;

generating a prediction envelope from a control biological dataset profile, which prediction envelope provides upper and lower limits for experimental variation;

wherein a test agent profile is considered to be different than the control if at least one parameter value of the profile exceeds the prediction envelope limits that correspond to a predefined level of significance.